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Figure 1 Nucleotide sequence alignment of LGR6.1 and LGR6.2 and LGR6.

LGR6.1	(1)	1	80
LGR6.2	(1)		
LGR6	(1)		
LGR6.1	(81)	81	160
LGR6.2	(81)		
LGR6	(63)		
LGR6.1	(161)	161	240
LGR6.2	(161)		
LGR6	(142)		
LGR6.1	(241)	241	320
LGR6.2	(241)		
LGR6	(222)		
LGR6.1	(321)	321	400
LGR6.2	(321)		
LGR6	(300)		
LGR6.1	(401)	401	480
LGR6.2	(401)		
LGR6	(300)		
LGR6.1	(481)	481	560
LGR6.2	(481)		
LGR6	(300)		
LGR6.1	(561)	561	640
LGR6.2	(561)		
LGR6	(300)		
LGR6.1	(641)	641	720
LGR6.2	(641)		
LGR6	(334)		
LGR6.1	(721)	721	800
LGR6.2	(721)		
LGR6	(414)		
LGR6.1	(801)	801	880
LGR6.2	(801)		
LGR6	(494)		
LGR6.1	(881)	881	960
LGR6.2	(881)		
LGR6	(574)		
LGR6.1	(961)	961	1040
LGR6.2	(961)		
LGR6	(654)		
LGR6.1	(1027)	1041	1120
LGR6.2	(1041)		
LGR6	(720)		

Figure 1 (cont.)

		1121		1200
LGR6.1	(1027)	-----	CTGCCCCCTAG	
LGR6.2	(1121)	-----	CTGCCCCCTAG	
LGR6	(720)	-----	CTGCCCCCTAG	
		1201		1280
LGR6.1	(1098)	-----	CTGCCCCCTAG	
LGR6.2	(1201)	-----	CTGCCCCCTAG	
LGR6	(791)	-----	CTGCCCCCTAG	
		1281		1360
6.1	(1178)	-----	CTGCCCCCTAG	
6.2	(1281)	-----	CTGCCCCCTAG	
GR6	(871)	-----	CTGCCCCCTAG	
		1361		1440
6.1	(1258)	-----	CTGCCCCCTAG	
6.2	(1361)	-----	CTGCCCCCTAG	
GR6	(951)	-----	CTGCCCCCTAG	
		1441		1520
6.1	(1338)	-----	CTGCCCCCTAG	
6.2	(1441)	-----	CTGCCCCCTAG	
GR6	(1031)	-----	CTGCCCCCTAG	
		1521		1600
6.1	(1418)	-----	CTGCCCCCTAG	
6.2	(1521)	-----	CTGCCCCCTAG	
GR6	(1111)	-----	CTGCCCCCTAG	
		1601		1680
6.1	(1498)	-----	CTGCCCCCTAG	
6.2	(1601)	-----	CTGCCCCCTAG	
GR6	(1191)	-----	CTGCCCCCTAG	
		1681		1760
6.1	(1578)	-----	CTGCCCCCTAG	
6.2	(1681)	-----	CTGCCCCCTAG	
GR6	(1271)	-----	CTGCCCCCTAG	
		1761		1840
6.1	(1658)	-----	CTGCCCCCTAG	
6.2	(1761)	-----	CTGCCCCCTAG	
GR6	(1351)	-----	CTGCCCCCTAG	
		1841		1920
6.1	(1738)	-----	CTGCCCCCTAG	
6.2	(1841)	-----	CTGCCCCCTAG	
GR6	(1431)	-----	CTGCCCCCTAG	
		1921		2000
6.1	(1818)	-----	CTGCCCCCTAG	
6.2	(1921)	-----	CTGCCCCCTAG	
GR6	(1511)	-----	CTGCCCCCTAG	
		2001		2080
6.1	(1898)	-----	CTGCCCCCTAG	
6.2	(2001)	-----	CTGCCCCCTAG	
GR6	(1591)	-----	CTGCCCCCTAG	
		2081		2160
6.1	(1978)	-----	CTGCCCCCTAG	
6.2	(2081)	-----	CTGCCCCCTAG	
GR6	(1671)	-----	CTGCCCCCTAG	
		2161		2240
6.1	(2058)	-----	CTGCCCCCTAG	
6.2	(2161)	-----	CTGCCCCCTAG	
GR6	(1751)	-----	CTGCCCCCTAG	

Figure 1 (cont.)

		2241	2320
LGR6.1	(2138)		
LGR6.2	(2241)		
LGR6	(1831)		
		2321	2400
LGR6.1	(2218)		
LGR6.2	(2321)		
LGR6	(1911)		
		2401	2480
LGR6.1	(2298)		
LGR6.2	(2401)		
LGR6	(1991)		
		2481	2560
LGR6.1	(2378)		
LGR6.2	(2481)		
LGR6	(2071)		
		2561	2640
LGR6.1	(2458)		
LGR6.2	(2561)		
LGR6	(2151)		
		2641	2720
LGR6.1	(2538)		
LGR6.2	(2641)		
LGR6	(2231)		
		2721	2800
LGR6.1	(2618)		
LGR6.2	(2721)		
LGR6	(2311)		
		2801	2880
LGR6.1	(2698)		
LGR6.2	(2801)		
LGR6	(2391)		
		2881	2960
LGR6.1	(2778)		
LGR6.2	(2881)		
LGR6	(2471)		
		2961	3040
LGR6.1	(2858)		
LGR6.2	(2961)		
LGR6	(2485)		
		3041	3120
LGR6.1	(2938)		
LGR6.2	(3041)		
LGR6	(2485)		
		3121	3200
LGR6.1	(3018)		
LGR6.2	(3121)		
LGR6	(2485)		
		3201	3280
LGR6.1	(3098)		
LGR6.2	(3201)		
LGR6	(2485)		
		3281	3360
LGR6.1	(3178)		
LGR6.2	(3281)		
LGR6	(2485)		

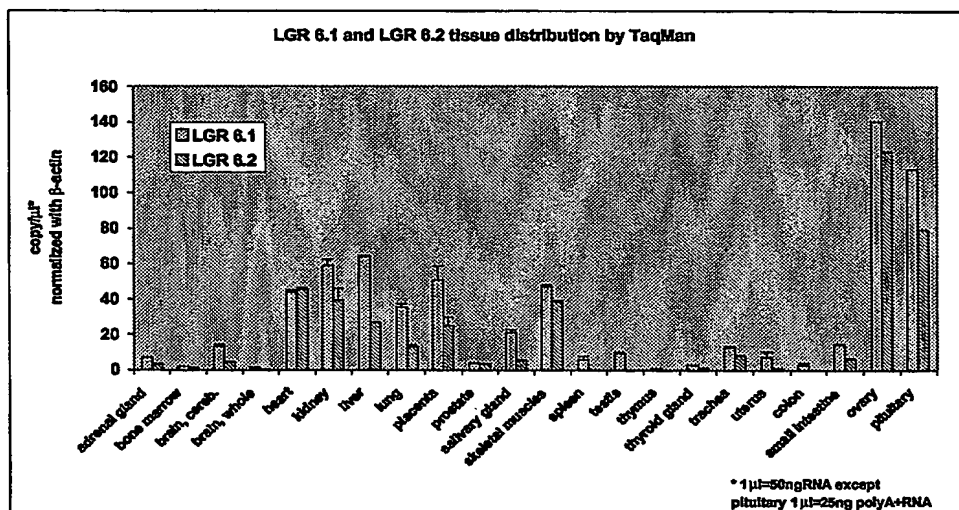
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Figure 1 (cont.)

		3361		3440
LGR6.1	(3258)	GAATAGCTTCTAAGGCTTC	AAAAAAAAAAAAAAAAAAAA	
LGR6.2	(3361)	GAATAGCTTCTGAGGCTTC	AAAAAAAAAAAAAAAAAAAA	
LGR6	(2485)			
		3441	3451	
LGR6.1	(3307)	-----		
LGR6.2	(3441)	AAAAAAAAAA		
LGR6	(2485)	-----		

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Figure 2



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Figure 3

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LGR6      MRLEGEGRSARAGQNLSPRAGSARRGAPRDLSMNNLTQLPGLFHHLRFLEELRLSGNHLS
LGR6.1    ---MGRPRLTLVCQ-VSIIISAR-----DLSMNNLTQLPGLFHHLRFLEELRLSGNHLS
LGR6.2    ---MGRPRLTLVCQ-VSIIISAR-----DLSMNNLTQLPGLFHHLRFLEELRLSGNHLS
          * . * : . * : *      ***      *****

LGR6      HIPGQAFSGLYSLKILMLQNNQLGGIPAEALWELPSLQSL -----
LGR6.1    HIPGQAFSGLYSLKILMLQNNQLGGIPAEALWELPSLQSLRLDANLISLVPERSFEGLS
LGR6.2    HIPGQAFSGLYSLKILMLQNNQLGGIPAEALWELPSLQSLRLDANLISLVPERSFEGLS
          *****

:6        -----
:6.1      LRHLWLDNALTEIPVRALNN LPALQAMTLALNRISHIPDYAFQNLTSLVVLHLHNNRIQ
:6.2      LRHLWLDNALTEIPVRALNNLPALQAMTLALNRISHIPDYAFQNLTSLVVLHLHNNRIQ

:6        -----DLNYNKLQEFFVAIRTLGRLQELGFHNNN IKAPEKAFMGNPLL
:6.1      HLGTHSFEGHNNLETLDLNYNKLQEFFVAIRTLGRLQELGFHNNNIKAPEKAFMGNPLL
:6.2      HLGTHSFEGHNNLETLDLNYNKLQEFFVAIRTLGRLQELGFHNNNIKAPEKAFMGNPLL
          *****

:6        QTIHFYDNPIQFVGRSAFYQLPKLHTLSLNGAMDIQEFFDLKGTTSLEILTLAGIRLL
:6.1      QTIHFYDNPIQFVGRSAFYQLPKLHTLSLNGAMDIQEFFDLKGTTSLEILTLAGIRLL
:6.2      QTIHFYDNPIQFVGRSAFYQLPKLHTLSLNGAMDIQEFFDLKGTTSLEILTLAGIRLL
          *****

:6        PSGMCQQLPRLRVLELSHNQIEELPSLHRCQKLEEIIGLQHNRIWEIGADTFSQLSSLQAL
:6.1      PSGMCQQLPRLRVLELSHNQIEELPSLHRCQKLEEIIGLQHNRIWEIGADTFSQLSSLQAL
:6.2      PSGMCQQLPRLRVLELSHNQIEELPSLHRCQKLEEMRS -----
          *****;

:6        DLSWNAIRSIHPEAFSTLHSLVKLDLTDNQLTTLPLAGLGGIMHLKLGKGNLALSQAFSKD
:6.1      DLSWNAIRSIHPEAFSTLHSLVKLDLTDNQLTTLPLAGLGGIMHLKLGKGNLALSQAFSKD
:6.2      -----GGLYFLEPPS-----
          *** . * .

:6        SFPKLRILEVP YAYOCCPYGMCASFFKASGQWEADLHLDDEESSKRPLGLLARQAENHY
:6.1      SFPKLRILEVP YAYOCCPYGMCASFFKASGQWEADLHLDDEESSKRPLGLLARQAENHY
:6.2      -----ARGAWSGARV-----
          * * * . . :

:6        DQDLDELQLEMEDSKPHPSVQCSPTP GEFKPCYLFESWGIRLAVWAIIVLLSVLCNGLVL
:6.1      DQDLDELQLEMEDSKPHPSVQCSPTP GEFKPCYLFESWGIRLAVWAIIVLLSVLCNGLVL
:6.2      -----

:6        LTVFAGGFVPLPPVKFVVGAIAGANTLTGISCGLLASVDALTFGQFSEYGARWETGLGCR
:6.1      LTVFAGGFVPLPPVKFVVGAIAGANTLTGISCGLLASVDALTFGQFSEYGARWETGLGCR
:6.2      -----

:6        ATGFLAVLGSEASVLLLTAAVQCSVSVSCVRAYGKSPSLGSVRAGVLGCLALAGLAAAL
:6.1      ATGFLAVLGSEASVLLLTAAVQCSVSVSCVRAYGKSPSLGSVRAGVLGCLALAGLAAAL
:6.2      -----

:6        PLASVGEYGASPLCLPYAPPEGQPAALGFTVALVMNSFCFLVVAGAYIKLYCDLP
:6.1      PLASVGEYGASPLCLPYAPPEGQPAALGFTVALVMNSFCFLVVAGAYIKLYCDLP
:6.2      -----

:6        EAVWDCAMVRHVAVLIFADGLLYCPVAFLSFASMLGLFPVTPPEAVKSVLLVVLPLPACLN
:6.1      EAVWDCAMVRHVAVLIFADGLLYCPVAFLSFASMLGLFPVTPPEAVKSVLLVVLPLPACLN
:6.2      -----

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Figure 3 (cont.)

LGR6	PLLYLLFNPHFRDDLRLRPRAGDSGPLAYAAAGELEKSSCDSTQALVAFSDVDLILEAS
LGR6.1	PLLYLLFNPHFRDDLRLRPRAGDSGPLAYAAAGELEKSSCDSTQALVAFSDVDLILEAS
LGR6.2	-----
LGR6	EAGRPPGLETYGFPSTLISCQQPGAPRLEGSHCVEPEGNHFGNPQPSMDGELLRAEGS
LGR6.1	EAGRPPGLETYGFPSTLISCQQPGAPRLEGSHCVEPEGNHFGNPQPSMDGELLRAEGS
LGR6.2	-----
36	TPAGGGLSGGGGFQPSGLALLHTY
36.1	TPAGGGLSGGGGFQPSGLAFASHV
36.2	-----

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Figure 4.

Domains within the query sequence LGR6 of 828 residues

1 100 200



Domains within the query sequence LGR6.1 of 915 residues

100 200



Domains within the query sequence LGR6.2 of 348 residues

100 200



transmembrane segments as predicted by the *TMHMM2* program (▨), coiled coil regions determined by *Coils2* program (▩) and Segments of low compositional complexity, determined by the *SEG* program (▨), signal peptides determined by the *SignalP* program (▨), GPI anchors are indicated by (▨). Regions containing repeats detected by *Prospero*, but not covered by domains are indicated by (▨).